



SEQUENCE LISTING

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<120> IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76

<130> 100337.54260US

<140> 10/628,464

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<170> PatentIn Ver. 3.2

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

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Ala Ile Ile Leu Val Thr Ile Leu Leu Leu Arg Leu Val Ala Ile
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gca ggc aat ggc ttc atc act gct gct ctg ggc gtg gag tgg gtg cta 144
Ala Gly Asn Gly Phe Ile Thr Ala Ala Leu Gly Val Glu Trp Val Leu
35 40 45

cgg aga atg ttg ttg cct tgt gat aag tta ttg gtt agc cta ggg gcc 192
Arg Arg Met Leu Leu Pro Cys Asp Lys Leu Leu Val Ser Leu Gly Ala
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tct cgc ttc tgt ctg cag tca gtg gta atg ggt aag acc att tat gtt 240
Ser Arg Phe Cys Leu Gln Ser Val Val Met Gly Lys Thr Ile Tyr Val
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ttc ttg cat ccg atg gcc ttc cca tac aac cct gta ctg cag ttt cta 288
Phe Leu His Pro Met Ala Phe Pro Tyr Asn Pro Val Leu Gln Phe Leu
85 90 95

gct ttc cag tgg gac ttc ctg aat gct gcc acc tta tgg tcc tct acc 336
Ala Phe Gln Trp Asp Phe Leu Asn Ala Ala Thr Leu Trp Ser Ser Thr
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Trp Leu Ser Val Phe Tyr Cys Val Lys Ile Ala Thr Phe Thr His Pro
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Ile Gly Asn His Arg Met Tyr Gln Asn Tyr Leu Arg Asn His Leu Gln			
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Pro Trp Asn Val Thr Gly Asp Ser Ile Arg Ser Tyr Cys Glu Lys Phe			
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tat ctc ttc cct cta aaa atg att act tgg aca atg ccc act gct gtc		624	
Tyr Leu Phe Pro Leu Lys Met Ile Thr Trp Thr Met Pro Thr Ala Val			
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ttt ttc att tgc atg att ttg ctc atc aca tct ctg gga aga cac agg		672	
Phe Phe Ile Cys Met Ile Leu Leu Ile Thr Ser Leu Gly Arg His Arg			
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aag aag gct ctc ctt aca acc tca gga ttc cga gag ccc agt gtg cag		720	
Lys Lys Ala Leu Leu Thr Thr Ser Gly Phe Arg Glu Pro Ser Val Gln			
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Ala His Ile Lys Ala Leu Leu Ala Leu Leu Ser Phe Ala Met Leu Phe			
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Ile Ser Tyr Phe Leu Ser Leu Val Phe Ser Ala Ala Gly Ile Phe Pro			
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Pro Leu Asp Phe Lys Phe Trp Val Trp Glu Ser Val Ile Tyr Leu Cys			
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Ala Gly Asn Gly Phe Ile Thr Ala Ala Leu Gly Val Glu Trp Val Leu
 35 40 45

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Ser Arg Phe Cys Leu Gln Ser Val Val Met Gly Lys Thr Ile Tyr Val
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 85 90 95

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 100 105 110

Trp Leu Ser Val Phe Tyr Cys Val Lys Ile Ala Thr Phe Thr His Pro
 115 120 125

Val Phe Phe Trp Leu Lys His Lys Leu Ser Gly Trp Leu Pro Trp Met
 130 135 140

Leu Phe Ser Ser Val Gly Leu Ser Ser Phe Thr Thr Ile Leu Phe Phe
 145 150 155 160

Ile Gly Asn His Arg Met Tyr Gln Asn Tyr Leu Arg Asn His Leu Gln
 165 170 175

Pro Trp Asn Val Thr Gly Asp Ser Ile Arg Ser Tyr Cys Glu Lys Phe
 180 185 190

Tyr Leu Phe Pro Leu Lys Met Ile Thr Trp Thr Met Pro Thr Ala Val
 195 200 205

Phe Phe Ile Cys Met Ile Leu Leu Ile Thr Ser Leu Gly Arg His Arg
 210 215 220

Lys Lys Ala Leu Leu Thr Thr Ser Gly Phe Arg Glu Pro Ser Val Gln
 225 230 235 240

Ala His Ile Lys Ala Leu Leu Ala Leu Leu Ser Phe Ala Met Leu Phe
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Ile Ser Tyr Phe Leu Ser Leu Val Phe Ser Ala Ala Gly Ile Phe Pro
 260 265 270

Pro Leu Asp Phe Lys Phe Trp Val Trp Glu Ser Val Ile Tyr Leu Cys
 275 280 285

Ala Ala Val His Pro Ile Ile Leu Leu Phe Ser Asn Cys Arg Leu Arg
 290 295 300

Ala Val Leu Lys Ser Arg Arg Ser Ser Arg Cys Gly Thr Pro
 305 310 315